



09655186

2/24	3/24
4/24	5/24
6/24	7/24

Fig.1



-60 tgaaaagatagaataaatggcctcgtg

1 ATGGCGCGGCCAGCGCTGCTGGGCGAG

1 M A R P A L L G E

61 GGCCAAGTTGCCGCGGCCACAGAAGTT

21 G Q V A A A T E V

121 GAAAATCTCTGCACGATAATATGGACG

41 E N L C T I I W T

181 ACTCTCAGATATTTTAGTCACTTTGAT

61 T L R Y F S H F D

241 CATCGTAAAGAGGAATTACCCCTGGAT

81 H R K E E L P L D

301 AGTGCCAATGAAAGTGAGAAGCCTAGC

101 S A N E S E K P S

361 GGTGATCCTGAGTCCGCTGTGACTGAG

121 G D P E S A V T E

421 AAGTGTTCTGCTCCCTGGAAGGAAT

141 K C S W L P G R N

Fig. 1A



ccgaattcggcacgagccgagggcgagggcctgc

CTGTTGGTGCTGCTACTGTGGACCGCCACCGTG

L L V L L L W T A T V

CAGCCACCTGTGACGAATTTGAGCGTCTCTGTC

Q P P V T N L S V S V

TGGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC

W S P P E G A S P N C

GACCAACAGGATAAGAAAATTGCTCCAGAACT

D Q Q D K K I A P E T

GAGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT

E K I C L Q V G S Q C

CCTTTGGTGAAAAAGTGCATCTCA

P L V K K C I S

P P E

CTCAAGTGCATTTGGCATAACCTGAGCTATATG

L K C I W H N L S Y M

ACAAGCCCTGACACACACTATACTCTGTACTAT

T S P D T H Y T L Y Y

Fig. 1B



481	TGGTACAGCAGCCTGGACAAAAGTCGT
161	W Y S S L E K S R
541	ATTGCTTGTTTCCTTTAAATTGACTAAA
181	I A C S F K L T K
601	ATAATGGTCAAGGATAATGCTGGGAAA
201	I M V K D N A G K
661	TCCTATGTGAAACCTGATCCTCCACAT
221	S Y V K P D P P H
721	TTAGTGCAGTGGAAGAATCCACAAAAT
241	L V Q W K N P Q N
781	GTCAATAATACTCAAACCGACCGACAT
261	V N N T Q T D R H
841	AATTCCGAATCTGATAGAAACATGGAG
281	N S E S D R N M E
901	GCCGACGCTGTCTACACAGTCAGAGTA
301	A D A V Y T V R V
961	AACAAACTGTGGAGTGATTGGAGTGAA
321	N K L W S D W S E



CAATGTGAAAACATCTATAGAGAAGGTCAACAC
Q C E N I Y R E G Q H

GTGGAACCTAGTTTTGAACATCAGAACGTTCAA
V E P S F E H Q N V Q

ATTAGGCCATCCTGCAAAATAGTGTCTTTAACT
I R P S C K I V S L T

ATTAAACATCTTCTCCTCAAAAATGGTGCCTTA
I K H L L L K N G A L

TTTAGAAGCAGATGCTTAACTTATGAAGTGGAG
F R S R C L T Y E V E

AATATTTTAGAGGTTGAAGAGGACAAATGCCAG
N I L E V E E D K C Q

GGTACAAGTTGTTTCCAACCTCCCTGGTGTTCCTT
G T S C F Q L P G V L

AGAGTCAAAACAAACAAGTTATGCTTTGATGAC
R V K T N K L C F D D

GCACAGAGTATAGGTAAGGAGCAAAACTCCACC
A Q S I G K E Q N S T



1021	<u>TTCTACACCACCATGTTACTCACCATT</u>
341	<u>F Y T T M L L T I</u>
1081	<u>CTTTTTTACCTGAAAAGGCTTAAGATC</u>
361	<u>L F Y L K R L K I</u>
1141	ATTTTAAAGAAATGTTTGGAGACCAG
381	I F K E M F G D Q
1201	ATCTATGAGAAACAATCCAAAGAAGAA
401	I Y E K Q S K E E
1261	AAAGCAGCTCCTTGAtggggagaagtg
421	K A A P *
1321	gatttattgcattctccatttggttatc
1381	cttgaaaaacaggcagctcctaagagc
1441	ccaaacccaaaggagctccttccaaga
1501	ccctaaaagcagatgttttgccaaatc
1561	accatcaattcatctaatacaggaattg

Fig. 1E



CCAGTCTTTGTCGCAGTGGCAGTCATAATCCTC
P V F V A V A V I I L

ATTATATTTCTCCAATTCCTGATCCTGGCAAG
I I F P P I P D P G K

AATGATGATACCCTGCACTGGAAGAAGTATGAC
N D D T L H W K K Y D

ACGGATTCTGTAGTGCTGATAGAAAACCTGAAG
T D S V V L I E N L K

atttcttttcttgccttcaatgtgaccctgtgaa

tgggggacttggttaaataagaaactgaaactact
cacaggtcttgatgtgacttttgcattgaaaac
aaagcaagagttcttctcgttccttggtccaat
cccaaactagaggacaaagacaaggggacaatg
tgatggcttcctaaggaatctctgcttgctctg

Fig. 1F

NR4 EXPRESSION IN MOUSE TISSUES

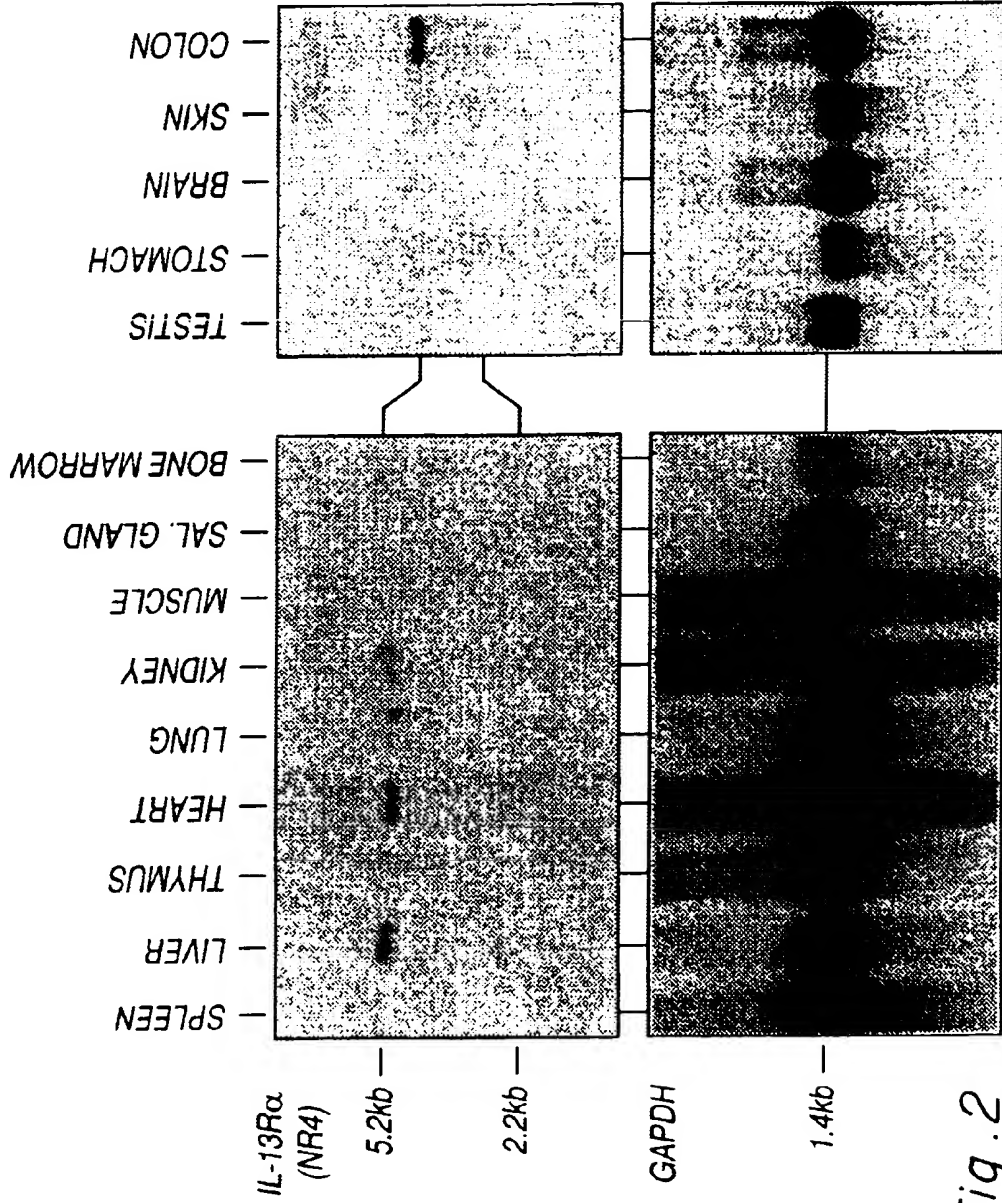


Fig. 2

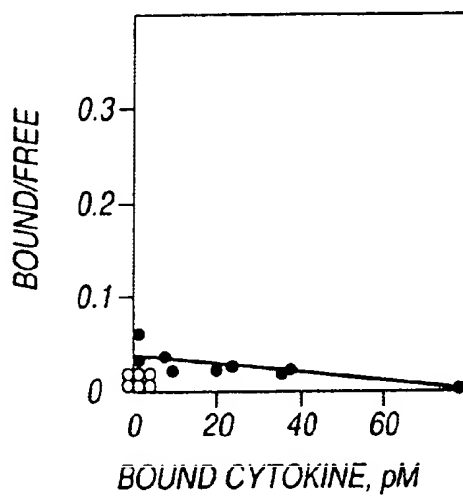


Fig. 3A

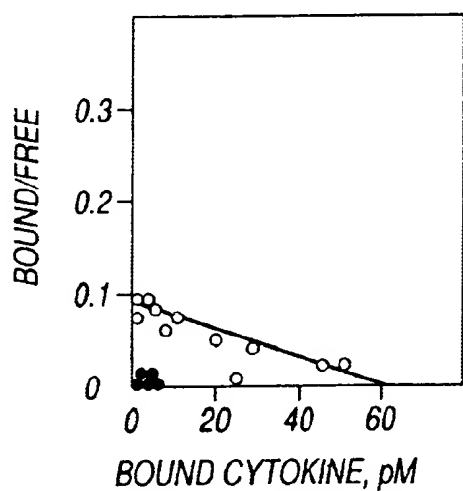


Fig. 3B

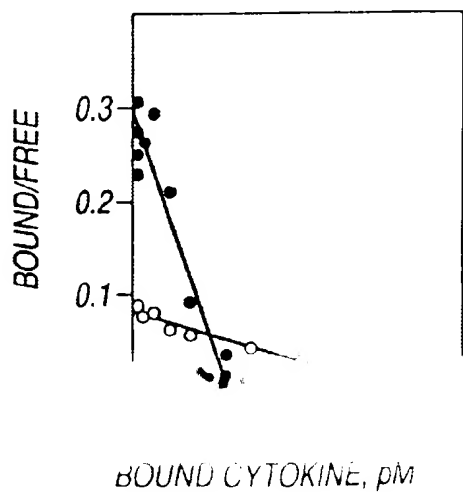


Fig. 3C

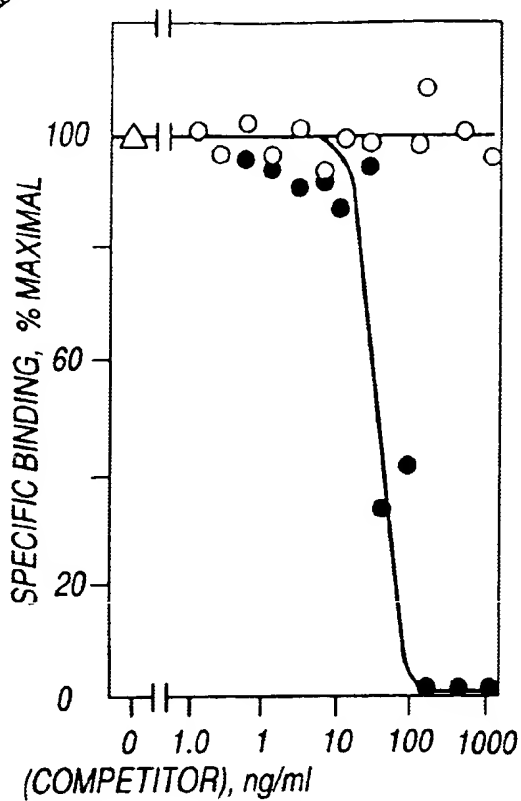


Fig. 4A

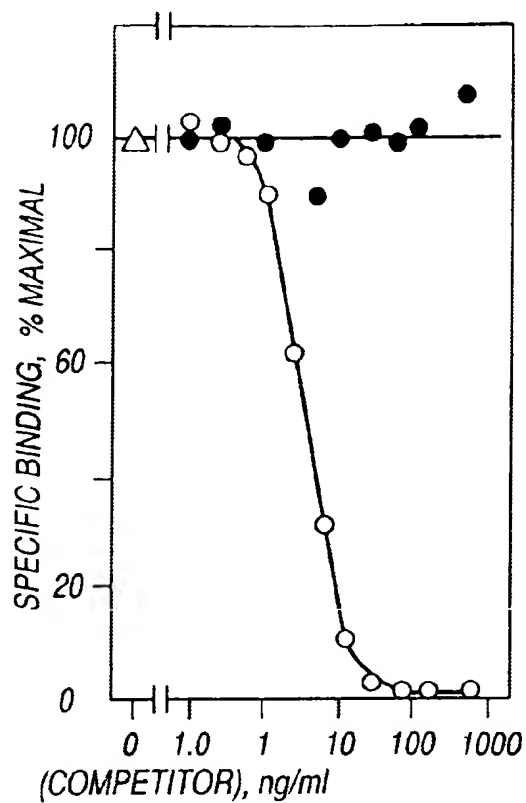


Fig. 4B

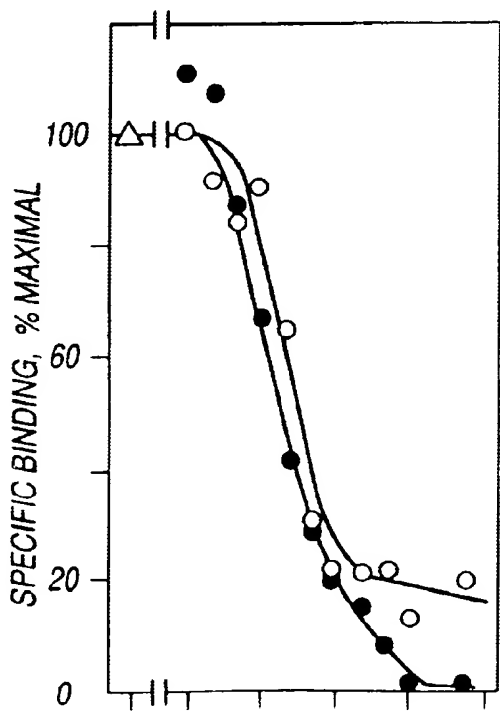


Fig. 4C

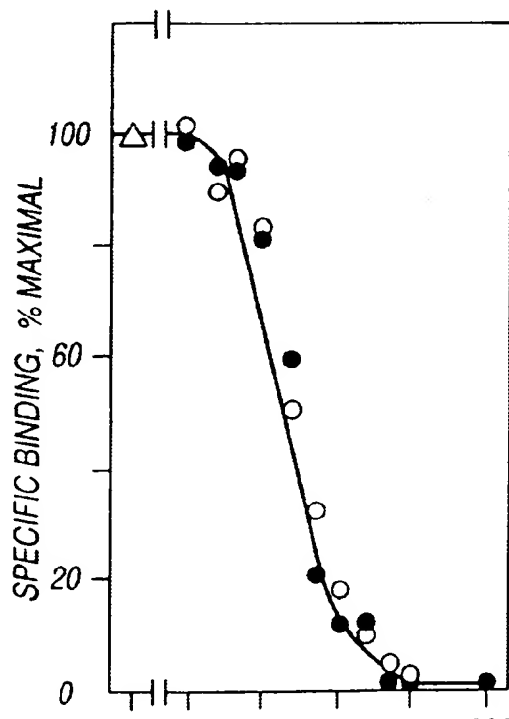


Fig. 4D

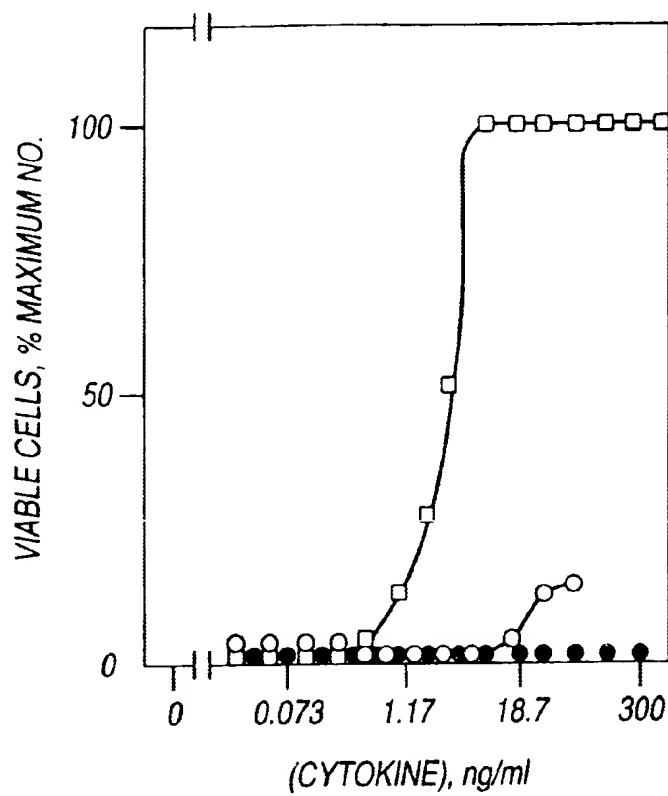


Fig. 5A

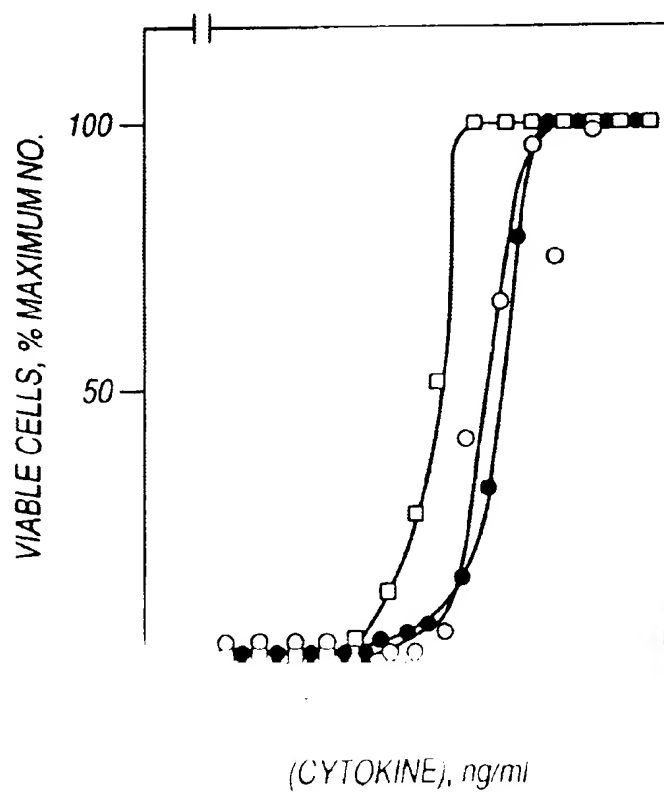


Fig. 5B



CROSS-SPECIES CONSERVATION OF THE NR-4 (IL-13R α) GENE

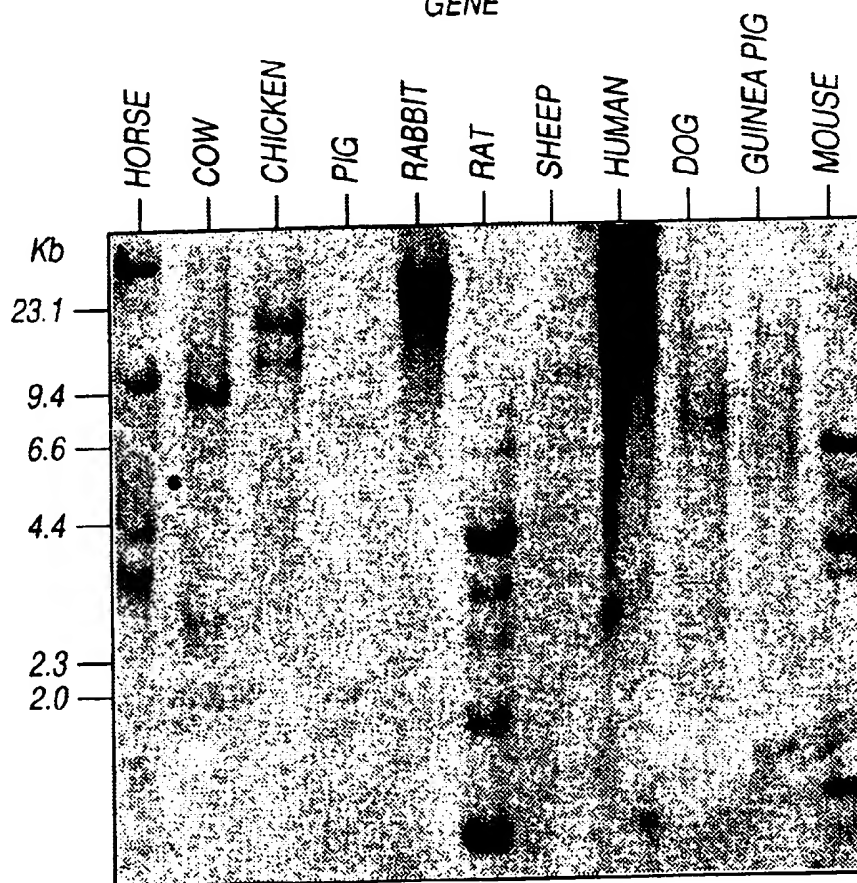


Fig. 6

(major)

DYKDD	DDYKD	DDESR	TEVQP	PVTXL	SV
1	5	10	15	20	25

(minor)

ASTSS	SDYKD	DDESR	TEVQP	PVTXL	SV
-------	-------	-------	-------	-------	----



14/24	15/24
16/24	17/24
18/24	19/24
20/24	21/24
22/24	23/24



H		gagtcctaacacggaccaaggagtttaac
M	- 60	tgaaaagatagaataaaatggcctcgtgc
H		M E W P A R L C G
		ATGGAGTGGCCGGCGCGGCTCTGCGGGC
		* * * *
M	1	ATGGCGCGGCCAGCGCTGCTGGGCGAGC
M	1	M A R P A L L G E
H		G G G G A P T E T
H		GGGGGCGGGGGCGCGCCTACGGAAACTC
		* * * *
M	61	GGCCAAGTTGCCGCGGCCACAGAAGTTC
M	21	G Q V A A A T E V
H		E N L C T V I W T
H		GAAAACCTCTGCACAGTAATATGGACAT
		* * * * * * * *
M	121	GAAAATCTCTGCACGATAATATGGACGT
M	41	E N L C T I I W T
H		S L W Y F S H F G
H		AGTCTATGGTATTTTAGTCATTTTGGCG
		* * * * *
M	181	ACTCTCAGATATTTTAGTCACTTTGATG
M	61	T L R Y F S H F D

Fig 7A



acgtgcggccgggttccgagggcgagaggctgc

.....

cgaattcggcacgagccgagggcgagggcctgc

L W A L L L C A G G G G
TGTGGGCGCTGCTGCTCTGCGCCGGCGGGGGGC

* * * *

TGTTGGTGCTGCTACTGTGGACCGCCACCGTG - - -

L L V L L L W T A T V -

Q P P V T N L S V S V
AGCCACCTGTGACAAATTTGAGTGTCTCTGTT

* * * * *

AGCCACCTGTGACGAATTTGAGCGTCTCTGTC

Q P P V T N L S V S V

W N P P E G A S S N C
GGAATCCACCCGAGGGAGCCAGCTCAAATTGT

* * * * *

GGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC

W S P P E G A S P N C

D K Q D K K I A P E T
ACAAACAAGATAAGAAAATAGCTCCGGAAACT

* * * * *

ACCAACAGGATAAGAAAATTGCTCCAGAAACT

D Q Q D K K I A P E T

Fig 7R



H		R R S I E V P L N
H		CGTCGTTCAATAGAAGTACCCCTGAATG
		* * * *
M	241	CATCGTAAAGAGGAATTACCCCTGGATG
M	81	H R K E E L P L D
H		S T N E S E K P S
H		AGCACCAATGAGAGTGAGAAGCCTAGCA
		* * * * *
M	301	AGTGCCAATGAAAGTGAGAAGCCTAGCC
M	101	S A N E S E K P S
H		G D P E S A V T E
H		GGTGATCCTGAGTCTGCTGTGACTGAAC
		* * * * *
M	361	GGTGATCCTGAGTCCGCTGTGACTGAGC
M	121	G D P E S A V T E
H		K C S W L P G R N
H		AAGTGTTCTTGGCTCCCTGGAAGGAATA
		* * * * *
M	421	AAGTGTTCTTGGCTCCCTGGAAGGAATA
M	141	K C S W L P G R N
H		W H R S L E K I H
H		TGGCACAGAAGCCTGGAAAAAATTCATC

Fig 7C



E R I C L Q V G S Q C
AGAGGATTTGTCTGCAAGTGGGGTCCCAGTGT
* * * * *
AGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT
E K I C L Q V G S Q C

I L V E K C I S P P E
TTTTGGTTGAAAAATGCATCTCACCCCCAGAA
* * * * *
CTTTGGTGAAAAAGTGCATCTCACCCCCTGAA
P L V K K C I S P P E

L Q C I W H N L S Y M
TTCAATGCATTTGGCACAACCTGAGCTACATG
* * * * *
TCAAGTGCATTTGGCATAACCTGAGCTATATG
L K C I W H N L S Y M

T S P D T N Y T L Y Y
CCAGTCCCGACACTAACTATACTCTCTACTAT
* * * * *
CAAGCCCTGACACACACTATACTCTGTACTAT
T S P D T H Y T L Y Y

Q C E N I F R E G Q Y
AATGTGAAAACATCTTTAGAGAAGGCCAATAC

Fig. 7D



		* * * * *
M	481	TGGTACAGCAGCCTGGAGAAAAGTCGTC
M	161	W Y S S L E K S R
H		F G C S F D L T K
H		TTTGGTTGTTTCCTTTGATCTGACCAAAG
		* * * * * *
M	541	ATTGCTTGTTTCCTTTAAATTGACTAAAG
M	181	I A C S F K L T K
H		Q I M V K D N A G
H		CAAATAATGGTCAAGGATAATGCAGGAA
		* * * * * * * * *
M	601	CAAATAATGGTCAAGGATAATGCTGGGA
M	201	Q I M V K D N A G
H		T S R V K P D P P
H		ACTTCCCGTGTGAAACCTGATCCTCCAC
		* * * * * * * *
M	661	ACTTCCTATGTGAAACCTGATCCTCCAC
M	221	T S Y V K P D P P
H		L Y V Q W E N P Q
H		CTATATGTGCAATGGGAGAATCCACAGA
		* * * * * * *
M	721	TTATTAGTGCAAGTGAAGAATCCACAAA
M	241	L L V Q W K N P Q

Fig 7F



* * * * *

AATGTGAAAACATCTATAGAGAAGGTCAACAC
Q C E N I Y R E G Q H

V K D S S F E Q H S V
TGAAGGATTCCAGTTTGAACAACACAGTGTC
* * * *

TGGAACCT - - - AGTTTTGAACATCAGAACG TT
V E P - S F E H Q N V

K I K P S F N I V P L
AAATTAAACCATCCTTCAATATAGTGCCTTTA
* * * * *

AAATTAGGCCATCCTGCAAAATAGTGTCTTTA
K I R P S C K I V S L

H I K N L S F H N D D
ATATTAAAACCTCTCCTTCCACAATGATGAC
* * * *

ATATTAAACATCTTCTCCTCAAAAATGGTGCC
H I K H L L L K N G A

N F I S R C L F Y E V
ATTTTATTAGCAGATGCCTATTTTATGAAGTA
* * * * *

ATTTTAGAAGCAGATGCTTAACCTTATGAAGTG
N F R S R C L T Y E V

Fig 7F



H		E	V	N	N	S	Q	T	E	T
H		GAAGTCAATAACAGCCAAACTGAGACAC								
		*	*	*	*		*	*		
M	781	GAGGTCAATAATACTCAAACCGACCGAC								
M	261	E	V	N	N	T	Q	T	D	R
H		E	N	P	E	F	E	R	N	V
H		GAGAATCCAGAATTTGAGAGAAATGTGG								
		*		*			*	*		
M	841	CAGAATTCCGAATCTGATAGAAACATGG								
M	281	Q	N	S	E	S	D	R	N	M
H		L	P	D	T	L	N	T	V	R
H		CTTCCTGATACTTTGAACACAGTCAGAA								
		*		*			*	*	*	
M	901	CTTGCCGACGCTGTCTACACAGTCAGAG								
M	301	L	A	D	A	V	Y	T	V	R
H		D	D	K	L	W	S	N	W	S
H		GATGACAAACTCTGGAGTAATTGGAGCC								
		*		*	*	*	*		*	*
M	961	GACAACAAACTGTGGAGTGATTGGAGTG								
M	321	D	N	K	L	W	S	D	W	S
H		T	L	Y	I	T	M	L	L	I
H		ACACTCTACATAACCATGTTACTCATTG								

H N V F Y V Q E A K C
ATAATGTTTTCTACGTCCAAGAGGCTAAATGT
* * * * *
ATAATATTTTAGAGGTTGAAGAGGACAAATGC
H N I L E V E E D K C

E N T S C F M V P G V
AGAATACATCTTGTTTCATGGTCCCTGGTGTT
* * * * *
AGGGTACAAGTTGTTTCCAACCTCCCTGGTGTT
E G T S C F Q L P G V

I R V K T N K L C Y E
TAAGAGTCAAAACAAATAAGTTATGCTATGAG
* * * * *
TAAGAGTCAAAACAAACAAGTTATGCTTTGAT
V R V K T N K L C F D

Q E M S I G K K R N S
AAGAAATGAGTATAGGTAAGAAGCGCAATTCC
* * * * *
AAGCACAGAGTATAGGTAAGGAGCAAAACTCC
E A Q S I G K E Q N S

V P V I V A G A I I V
TTCCAGTCATCGTCGCAGGTGCAATCATAGTA

Fig 7H

		*	*	*	*	*	*
M	1021	ACCTTCTACACCACCATGTTACTCACCA					
M	341	T F Y T T M L L T					
H		L L L Y L K R L K					
H		CTCCTGCTTTACCTAAAAAGGCTCAAGA					
		* * * * *					
M	1081	CTCCTTTTTTACCTGAAAAGGCTTAAGA					
M	361	L L F Y L K R L K					
H		K I F K E M F G D					
H		AAGATTTTTTAAAGAAATGTTTGGAGACC					
		* * * * *					
M	1141	AAGATTTTTTAAAGAAATGTTTGGAGACC					
M	381	K I F K E M F G D					
H		D I Y E K Q T K E					
H		GACATCTATGAGAAGCAAACCAAGGAGG					
		* * * * *					
M	1201	GACATCTATGAGAAACAATCCAAAGAAG					
M	401	D I Y E K Q S K E					
H		K K A S Q *					
H		AAGAAAGCCTCTCAGTGAtggagataat					
		* * *					
M	1261	AAGAAAGCAGCTCCTTGAtgggggagaag					
M	421	K K A A P *					

Fig. 7I



* * * * *

TTCCAGTCTTTGTCGCAGTGGCAGTCATAATC
I P V F V A V A V I I

I I I F P P I P D P G
TTATTATATTCCCTCCAATTCCTGATCCTGGC
* * * * *
TCATTATATTTCCCTCCAATTCCTGATCCTGGC
I I I F P P I P D P G

Q N D D T L H W K K Y
AGAATGATGATACTCTGCACTGGAAGAAGTAC
* * * * *
AGAATGATGATACCCTGCACTGGAAGAAGTAT
Q N D D T L H W K K Y

E T D S V V L I E N L
AAACCGACTCTGTAGTGCTGATAGAAAACCTG
* * * * *
AAACGGATTCTGTAGTGCTGATAGAAAACCTG
E T D S V V L I E N L

ttatattttaccttcactgtgaccttgagaaga

tgattttctttcttgccttcaatgtgaccctgt

Fig.7J

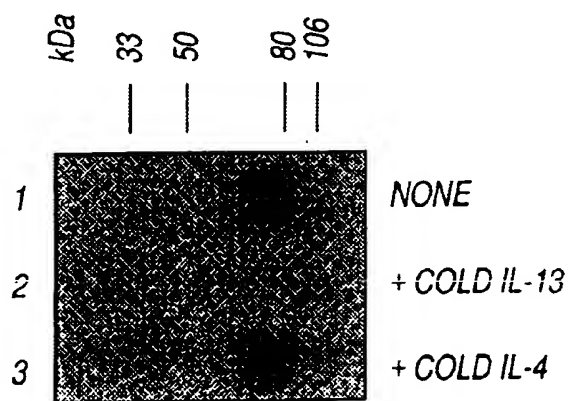


Fig.8

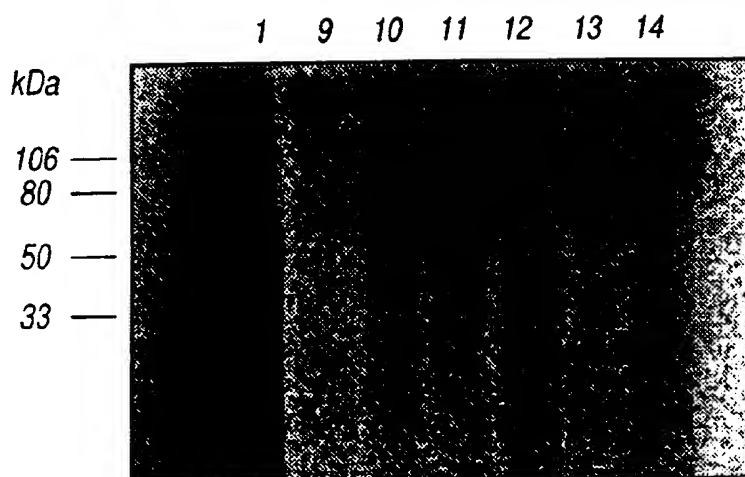


Fig.9